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# HABITAT TYPE AND CLIMATIC ZONE CORRELATE WITH GENOME SIZE VARIATION IN OSTEICHTHYES FISHES

**BINOD REGMI[1] & BASANTA RAJ WAGLE[2]**

[1]*Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas, USA*

[2] *Department of Poultry Science, University of Arkansas, Fayetteville, Arkansas, USA*

***ABSTRACT***

***Cytogenetic and environmental factors have been reported to cause variations in the genome size within the species. However, the broad scale genome size variation of a class of vertebrate especially Osteichthyes fishes across the different climatic zone and habitat conditions hasyet to be documented. In this study, we analyzed the genome size variation of 285 species of Osteichthyes fishes distributed across the marine and freshwater habitat. We found that habitat and climatic zone showed a significant pattern of genome size variation, however, the body size, chromosome number and diversity rate has no strong correlation with the genome size.***

***KEYWORDS: C-Value, Genome Size Variation, Osteichthyes, Climatic Zone, Marine Fish & Freshwater Fish***

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## INTRODUCTION

Among eukaryotes, the number of genes does not correlate with genome size. The discordant between organisms' complexity and genome size is called C-value paradox, a highly debated topic among geneticists and evolutionary biologists (Pagel & Johnstone, 1992). The variation in genome size has been correlated with several cytogenetic and phenotypic traits such as body size (Jeffery et al., 2016; McLaren et al.,1988), cell size, chromosome numbers (Clark et al., 2016), genome duplication (Clark et al., 2016), pseudogenes, embryonic development time (Jockusch, 1997), rate of basal metabolism (Vinogradov et al., 1995) and length or abundance of microsatellite genes (Crollius et al., 2000).Newer species with high diversity rates have smaller genome size than older species from deeper lineage in phylogenetic tree (Jeffery et al., 2016). Extrinsic environmental factors including temperature (McLaren et al., 1988), latitude, salinity, water depth (Jeffery et al., 2016), diet specialty, host type and distribution range (Calatayud et al., 2016)act as a selective force for genomic variation. The most convincing findings after advent of next generation sequencing data is the percentage of transposons in the genome that causes genome size variation among species (Sessegolo et al., 2016; Muñoz-López et al., 2010). The amplification and deletion of repetitive sequences in the genomescould change the fitness of an organism either through change in genome sequence or in physiological parameters of cell itself due to the size of the genome (Canapa et al., 2015).

Genome duplication and insertion-deletion of transposable elements are two main cytogenetic mechanisms of genome size variation but several other intrinsic and extrinsic factors are also responsible for these variations. Previously, Purcell et al. (2012) and Regmi and co-workers (2016) described the higher level of gene flowin aquatic vertebratesresiding in the coastal regions compared to that of freshwater habitat having the same

level of salinity and causing population differentiation and local adaptation. Such heterogenetic environment may accelerate the genomic variation due to selective pressure acting differently in different environment. It has been proposed that several environmental stressors induce insertion and deletion of transposons (Canapa et al., 2015; Hessen et al., 2013). Several studies have determined the cytogenetic and environmental factors that contribute to genome size variations in plants and animals, however, few studies have investigated the broad pattern of genome size variation across the families and orders of a class of vertebrate thriving in heterogeneous environment.

In this study, we have analyzed genome size variation of Osteichthyes fishes, a class of bony fish comprising diverse orders and families including the fishes from deep-sea habitat to extreme temperature and hypoxic condition like in the Tibetan plateau. Compiling a wide range of publicly available data set; we have asked whether the genome size variation is explained by climatic zone (tropical/temperate/artic), salinity (marine/freshwater), chromosome number, diversity (number of species of within a genus) and body size.

## METHODS

The estimated genome size and chromosome number of more than 286 species under 49 families were compiled from genome size database (www.genomesize.com) and published literature. Most of the genome size (pg $N^{-1}$or C- value) estimates were performed with Fenlgen densitometry and flow cytometry methods anda very few with bulk furometric assay. All the estimates were taken from genomes of red blood cells.

The larger genome size and the higher intergeneric variation in chondrichthyans (i.e. skates, sharks, and rays) have been previously recorded (Hardie & Hebert, 2004).Since this class of fish represents more primitive clade and dominants in the marine habitat, we have excluded itand also all the fishes that are primitive to chondrichthyansto avoid biases. We compiled the data of diversity rate, habitat type (marine/freshwater), range of distribution (tropical/subtropical/temperate) and standard body length from the fish base (www.fishbase.org)and published scientific literature. The diversity rate included the number of species recorded within the same genus. The standard body length was the length of a fish from tip of the snout to the last vertebra at the base of caudal fin. If the fish is distributed in marine or coastal habitat in any stage of its life history, it is classified as a marine.

The statistical analyses were performed in R program. We carried out univariate analysis of chromosome number and genome size. Mann-Whiteny- Wilcoxon test was conducted to investigate the association of genome size with marine and freshwater fishes after sorting the response variable (C-value). We used Kruskal-Wallis test to investigate the genome size variation based on broad climatic zone i.e. tropical, subtropical and temperate. We were unable to compile the data set for Arctic and Antarctic zones due to limited availability of the data. The association of genome size with body size, chromosome number and diversity rate were evaluated with Kendall tau rank correlation coefficient.

## RESULTS AND DISCUSSIONS

The distribution of response variable (C-value) meets the assumption of normality, however, the chromosome number has bimodal distribution with a major peak at fifty and a minor peak at hundred. This distribution showed a small signature of whole genome duplication in the studied samples. The diversity rate and body size were over-dispersed with single tail resembling a Poisson's distribution (Figure 1).

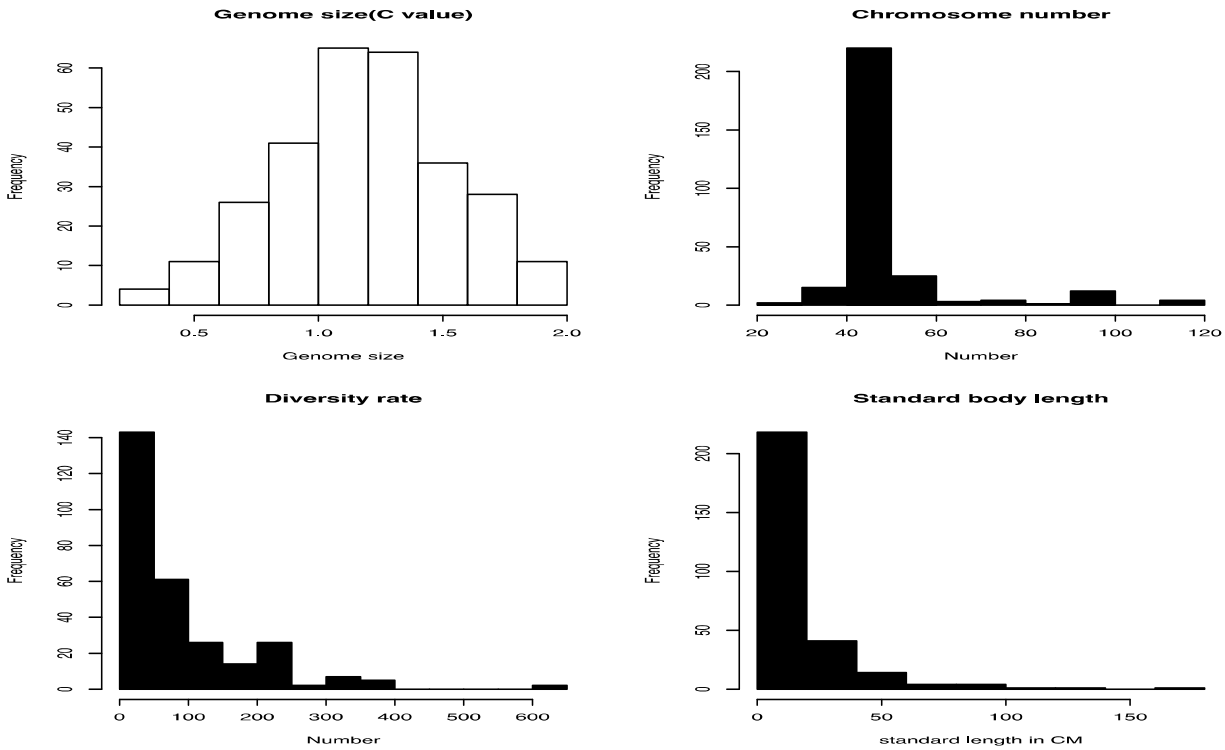


**Figure 1: Genome Size, Chromosome Number, Diversity Rate and Standard Body Length of Osteichthyes Fishes**

Wilcoxon rank test of genome size with habitat type showed that marine and freshwater fishes are not-identical (w=75673, $p$<0.001). We found larger genome size in freshwater fishes than their marine counterparts. There are several reasons of having a smaller genome size in marine as compared to freshwater fishes. Marine habitat represents a more stable systemand an absence of barriers could result in gene flow equilibrium that resists the genome size evolution. In contrast to this, the freshwater habitats are more prone to isolation and a high fluctuation of ecological factors could restrictthe gene flow. In such a heterogeneous environment, natural selection could favor larger genome size (Leinaas et al., 2016).

Kruskal-Wallis test of genome size variation across the climatic zone was also significant ($\chi^2$ = 7.41, df=2, $p$=0.02). Our data showed the increased trend of genomic content from tropical to temperate fishes. The present result that larger genome size in the temperate hantropical zone supports the previousfinding that cold water poikilotherms have larger genomes than that of warm water (Leinaas et al., 2016; Xia 1995). However, this result contradicts with the findings of Hardieand Herbert (2004), they reported the smaller genome size in cold water fishes. The smaller genome size of some artic fishes could potentially masks the general trend of genome size variation from tropical to temperate environment in Hardie and Herbert's finding.

In our study, Kendall's tau coefficients were weak for diversity rate ($t$ = 0.08), body size ($t$ = 0.11) and chromosome number ($t$ = 0.40).In a closely related ectotherms, thelarger body size in colder temperatures could be attributed to larger cell size, larger genome size and higher metabolic rate (Hessen et al., 2013). However, we did not find such association of body size and genome size in Osteichthyes fishes while looking at a broad pattern of variation across several orders and families.

## CONCLUSIONS

Our data captured the significant correlation of genome size with habitat condition and climatic zone. Looking at this broad pattern of variation, we can further pinpoint that the salinity and temperature could be the important environmental stressors that can manipulate transposons responsible for these variations. Further evaluation of the role of these stressors in control environment for multiple generations is warranted to confirm their contribution in genome size variation in natural populations.

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